

(1/13)

sp	P53350	-----MS-AAVTAGKLARA-----PADPGKAGVPGVAAPG---APAAAP
sp	Q9NYY3	MELLRTITYQPAASTKMCEQALGKGCADSKKKRPPQPPEESQPPQSQAVPPAAPHHHH
sp	Q9H4B4	-----MEPAAG-FLSPRPFORTAAATA---PPAGPG---PPPSALRGPELEMLAGL
		:. . . * : * * *
sp	P53350	PAKEIP---EVLVDPRSRRRYVRGRFLGKGGFAKCFEISDADTKEVFAGKIVPKSLLLK
sp	Q9NYY3	HHSMSGPEISRIIVDPTTGKRYCRGKVLGKGGFAKCYEMTDLTNNKVYAAKI I PHSRVAK
sp	Q9H4B4	PTSDPG---RLITDPRSGRITYLKGRLGKGGFARCYEATDTETGSAYAVKVIQSRVVK
		. . . : * : * : * : * : * : * : * : * : * : * : * : *
sp	P53350	PHOREKMSMEISIHRSIAHQHVGFHGFEDNDFVFFVLELCRRRSLELHKKRRKALTEP
sp	Q9NYY3	PHOREKIDKEIELHRI LHHKHVVQFYHYFEDKENIYILLEYCSRRSMAHILKARKVLTEP
sp	Q9H4B4	PHOREKILNEIELHRDLQHRHIVRFSSHFFEDADNIYIFLELC SRKSLAHIWKARHTLLEP
		*****: * : * : * : * : * : * : * : * : * : * : * : * : * : *
sp	P53350	EARYYLRQIVLGCQYLHRNRVHRLDLKLGFLNEDLEVKGIDFGLATKVEYDGERKKT
sp	Q9NYY3	EVRYYLRQIVSGLKYLHEQEILHRDLKLGFFINEAMELVGDFGLAARLEPLEHRRRTI
sp	Q9H4B4	EVRYYLRQILSGLKYLHQRGILHRDLKLGFFITENMELKVGDFGLAARLEPPEQRKTI
		*.*****: * : * : * : * : * : * : * : * : * : * : * : * : * : *
sp	P53350	CGTPNYIAPEVLSKKGHSFEVDVWSIGCIMYTLVVGKPPFETSCCLKETYLRICKNEYSIP
sp	Q9NYY3	CGTPNYLSPEVLNKGHGCESDI WALGCVMYTMLLGRPPFETTNLKETYRCIREARYTMP
sp	Q9H4B4	CGTPNYVAPEVLLRQGHGPEADVWSLGCVMYTLGCGSPPFETADLKETYRCIKQVHYTLP
		*****: * : * : * : * : * : * : * : * : * : * : * : * : * : *
sp	P53350	KHINPVAASLIQKMLQTDPTARPTINELLNDEFFTSGYIPARLPIT-CLTIP-----PR
sp	Q9NYY3	SSLLAPAKHLIASMLSKNPEDRPSLDDIIRHDFFLQGFTPDRLSSSCCHTVPDFHLSSPA
sp	Q9H4B4	ASLSLPARQLLAAILRASPRDRPSIDQILRHDFFTKGYTPDRLPISSCVTVPDLTTPNPA
		: * * : * : * : * : * : * : * : * : * : * : * : * : *
sp	P53350	---FSIAPSSLDPSNRK-----P---LTVLNKGLNLP---LPER-----
sp	Q9NYY3	KNFFFKAAAALFGGKKDKARYIDTHNRVSKEDEDIYKLRHDLKKT SITQPSKHRTPDEEL
sp	Q9H4B4	RSLFAKVTKSLFVRKKK-----SKNHAQERDE-VSGLVSGLMRTSVGHQDAR-----
		* . . : * : . : * : * : * : * : * : * : * : * : *
sp	P53350	--PRE---KEEPVVR-ET-----GEVVDCHLSMDLQQLHSVNASKPSEGLVR
sp	Q9NYY3	QPPTTTVARSGTPAVENKQOIGDAIRMIVRGTLGSCSSSECCLEDSTMGSVADTVARVLR
sp	Q9H4B4	--PEAPAASGPAPVSLVETAPEDSS---PRGTLASSGHG--FEEGLTVATVVESALCALR
		* . : * : * : * : * : * : * : * : * : * : * : *
sp	P53350	--QEEAEDPACIP-----IFWVSKWVDYSDKYGLGYQLCDNSVGVLFNDSRILILYN
sp	Q9NYY3	GLENMPEADCIPKEQLSTS-FQWVTKWVDYSNKYGFGYQLSDHTVGVLFNNGAHMSLLP
sp	Q9H4B4	NCIAFMPPAEQNPAPLAQPEPLVWFSEWVGFSNKFYGYQLSSRRVAVLFNDGTHMALSA
		. * : * : * : * : * : * : * : * : * : * : * : *
sp	P53350	DGDSLQYIERDGTESYLTVSSHPSNLMKKITLLKYFRNYMSEHLLKAGANITPREGDELA
sp	Q9NYY3	DKKTVHYAELGQCSVFPATDAPEQFISQVTVLKYFSHYMEENLMDGG-DLPSVTDIRRP
sp	Q9H4B4	NRKTVHYNPTSTKHFSFVGAVRRALQPQLGILRYFASYMEQHLMKGG-DLPSVEEVEVP
		: . : * : . . : : * : * : * : * : * : * : *
sp	P53350	RLPYLRTWFRTRSAILHLSNGSVQINFFQDHTKLILCP--LMAAVTYIDEKRDFRTYRL
sp	Q9NYY3	R-LYLLQWLKSDKALMMLFNDGTQVNFYHDHTKIIICSQNEEYLLTYINEDRISTTFRL
sp	Q9H4B4	APPLLLQWVKTDQALLMLFSDGTQVNFYGDHTKLILSG-WEPLLVTFVARNRSACTYLA
		* * : . : * : * : * : * : * : * : * : * : * : *
sp	P53350	SLLEEYGCCKELASRLRYARTMVDKLLSSRSASNRLKAS
sp	Q9NYY3	TTLLMSGCSELKNRMEYA-----LNMLLQRCN-----
sp	Q9H4B4	SHLRQLGCSPLRQRLRYA-----LRLLRDRSPA-----
		: * * : * : * : * : * : * : * : * : *

FIGURE 1

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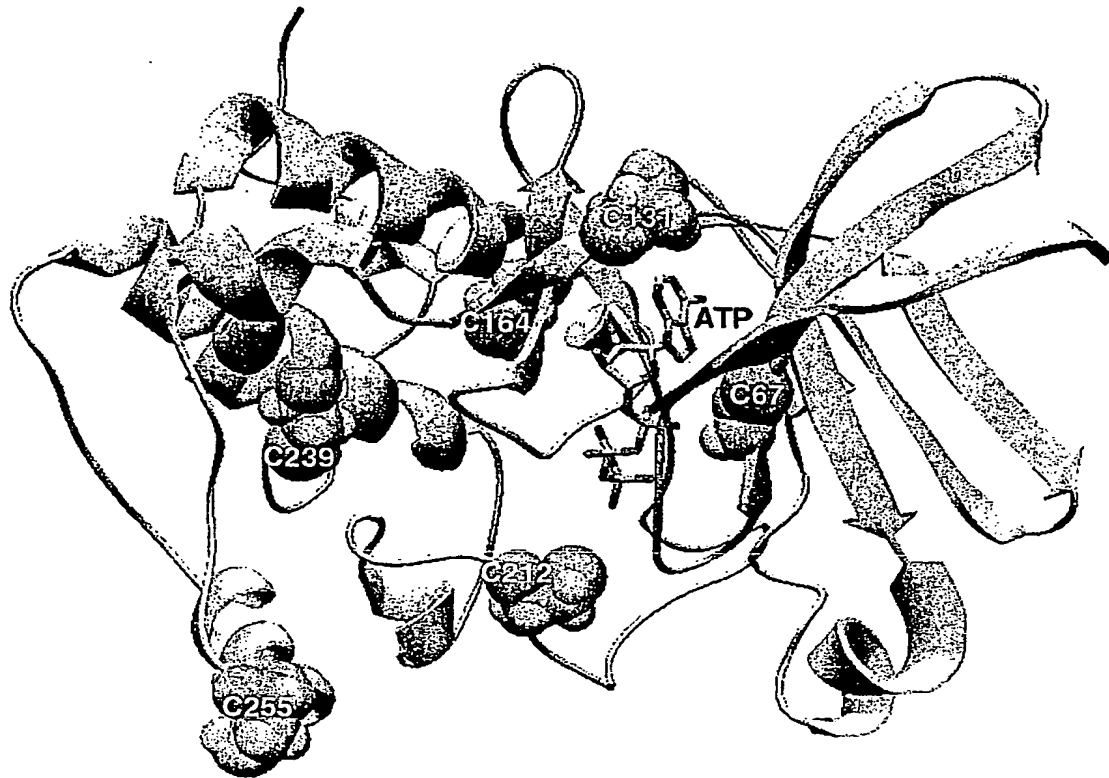


FIGURE 2

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1	MSAAVTAGKLARAPADPGKAGVPGVAAPGAPAAAPPAKE---	IPEVLVDP	47	PLK1
		. ...   ....  :. . ...		
1	MGNAAAAKKGSEQESVKEFLAKA		23	PKA
48	RS-----RRRYVRGRFLGKGGAFAKCFEISDADTKEVFAGK		82	PLK1
	:. :... ...  . . .....: ... .			
24	KEDFLKKWESPAQNTAHLDOFERIKTLGTGSFGRVMLVKHKETGNHYAMK		73	PKA
83	IVPKSLLLKPHQREKMSMEISTHRS LAHQHVVGFGFFEDNDFVFWLEL		132	PLK1
	: ...: .. . .... .. :.....: .... : ...: : .			
74	ILDKQKVVKLKQIEHTLNEKRILQAVNFPFLVKLEFSFKDNSNLYMVMEY		123	PKA
133	CRRRSLLLELHKRRKALTEPEARYYLROQIVLGCOQYLHRNRVTHRDLKLGNL		182	PLK1
	.....: .....: ..  : ..   ...: ...: : ... ..			
124	VPGGEMFSLHRRIGRFSEPHARFYAAQIVLTFEYLHSLDLTYRDLKPENL		173	PKA
183	FLNEDLEVKIGDFGLATKVEYDGERKKTLOGTPNYIAPEVLSKKGHSFEV		232	PLK1
	.....: ... .: : . ..   ... .: ...: ... : ...			
174	LIDQQGYIQVTDGFAKRVK---GRTWTLCGTPEYLAPETILSKGYNKAV		220	PKA
233	DVWSIGCIMYTLIVGKPPFETSCLKETYLRIKKNEYSIPKHINPVAASLI		282	PLK1
	.: : .: .: ... .. .....: .: .....: .: .....: :			
221	DWWALGVLIYEMAAGYPFFADQPIQIYEKIVSGKVRFPSPHFSSDLKDLL		270	PKA
283	QKMLQTDPTAR-----PTINELLNDEFF-TSGYIPARLPITCLTIPPRFS		326	PLK1
	:.: ... .: ..  :.: :..: .:   :..: .....: : .			
271	RNLLQVDLTKRFGNLKNGVNDIKNHKWFATTDWIAIYQRKVEAPFIPKFK		320	PKA

FIGURE 3

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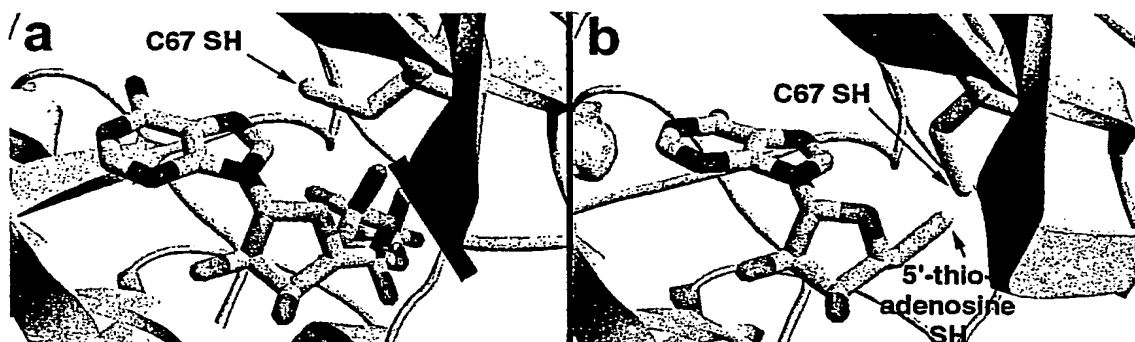


FIGURE 4

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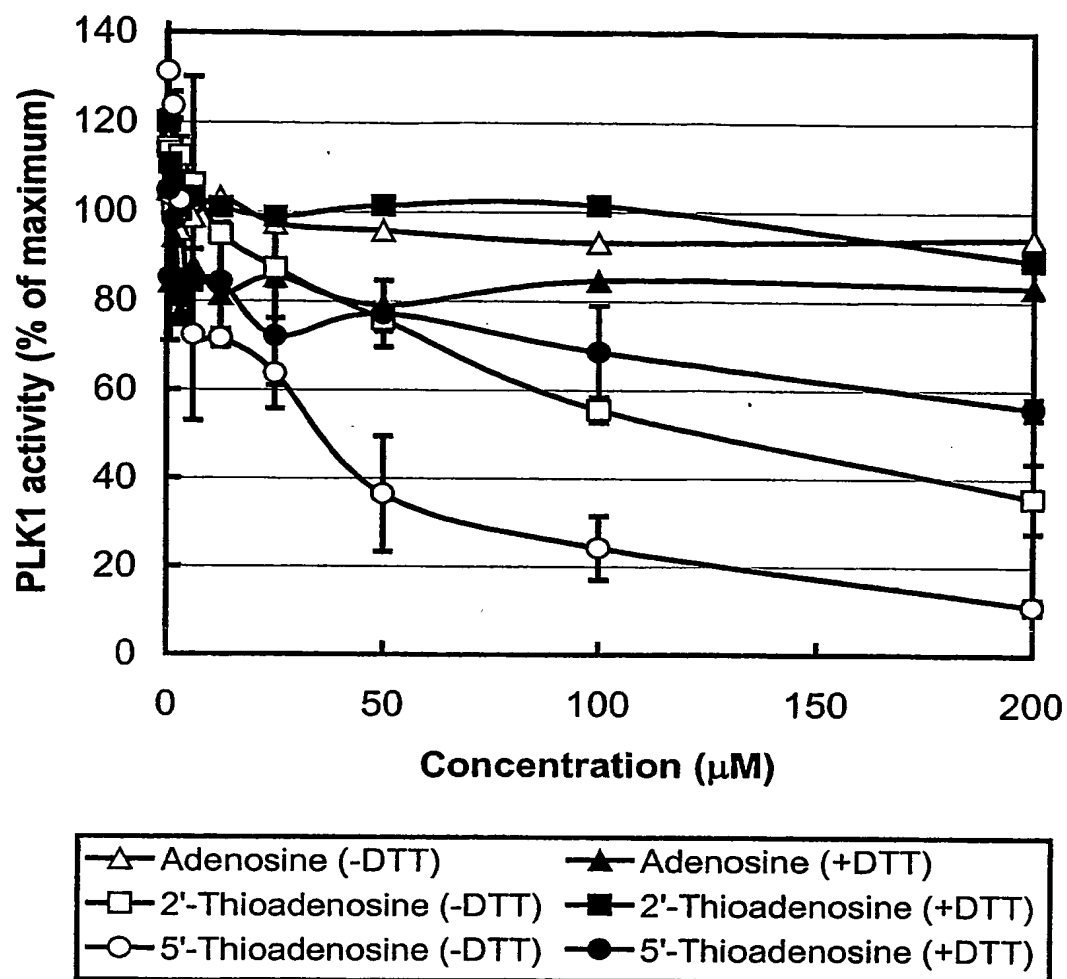


FIGURE 5

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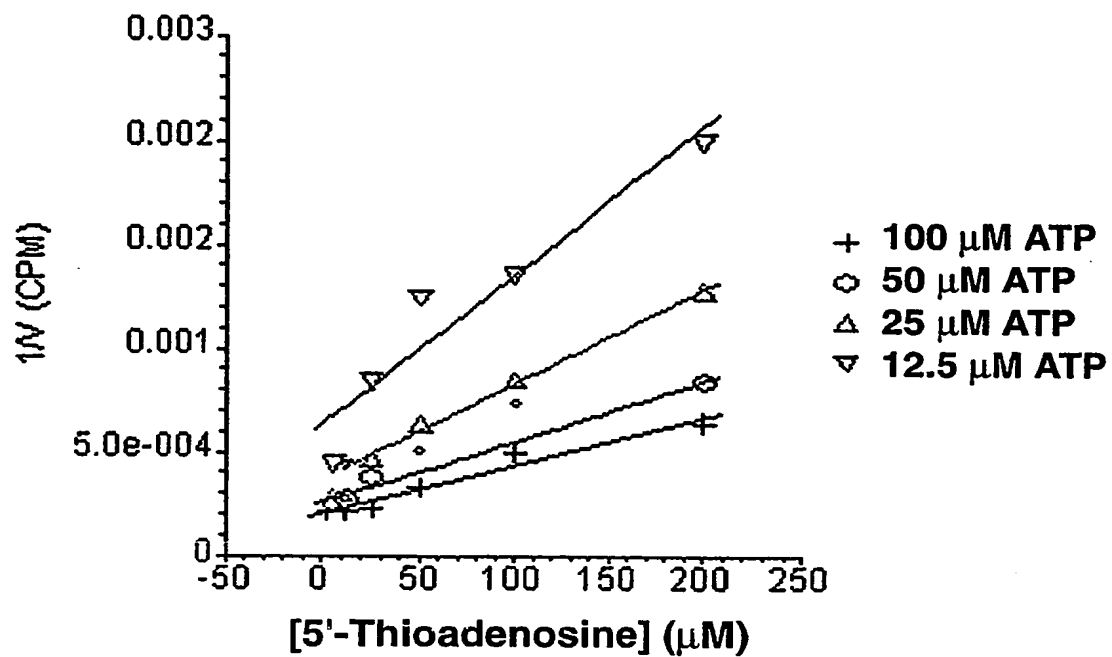
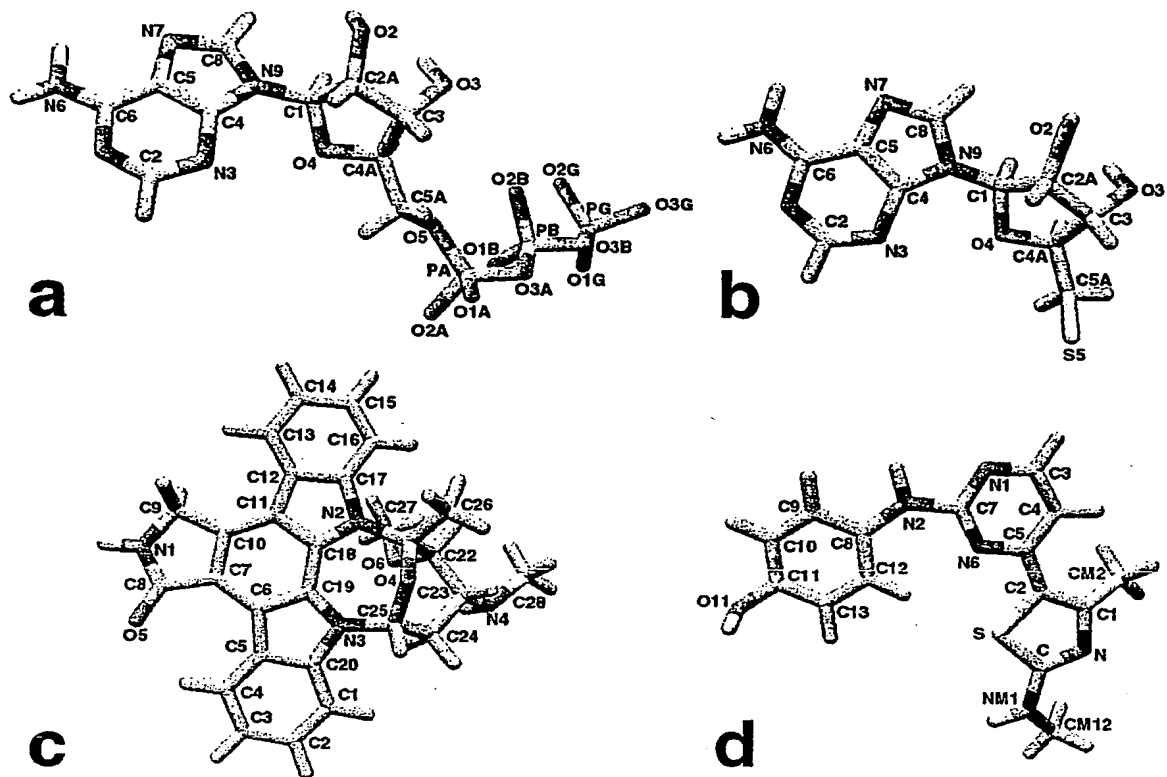


FIGURE 6

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### FIGURE 7

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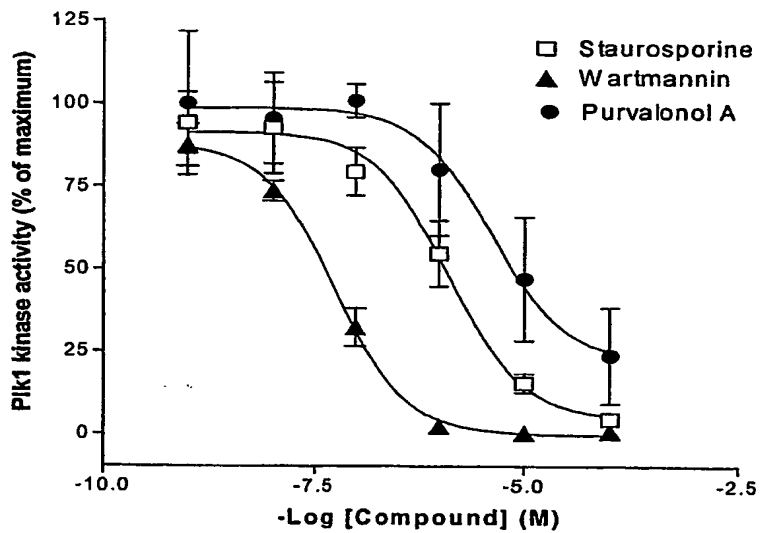


FIGURE 8

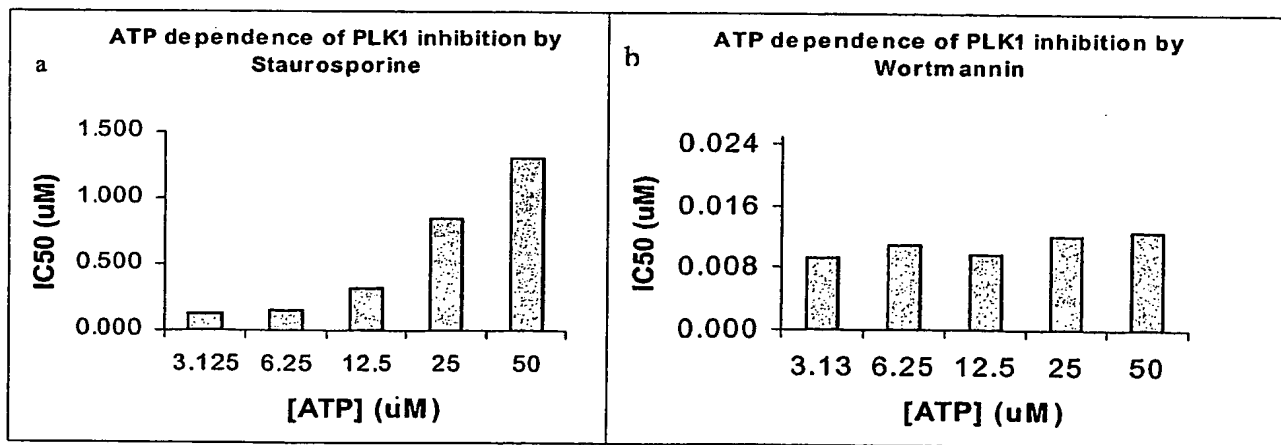


FIGURE 9



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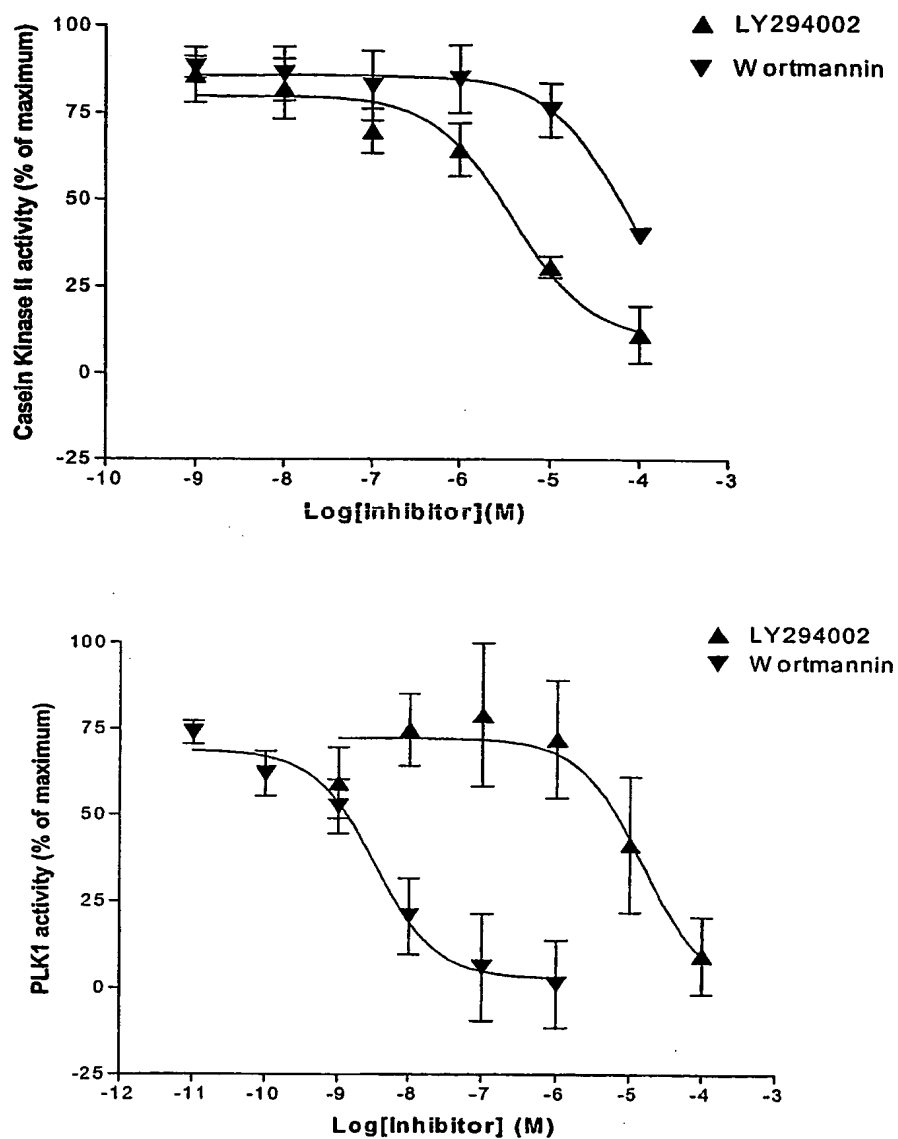


FIGURE 10

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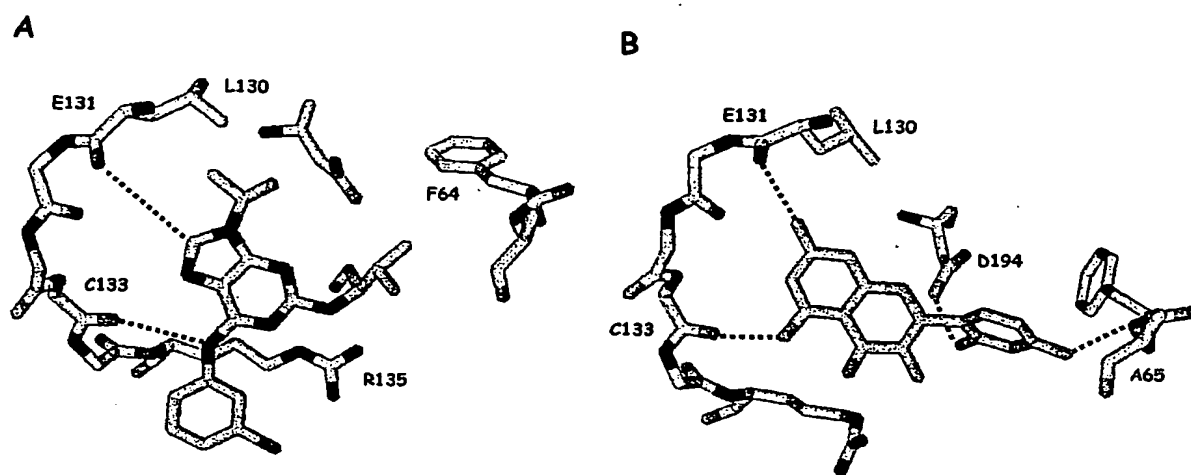


FIGURE 11

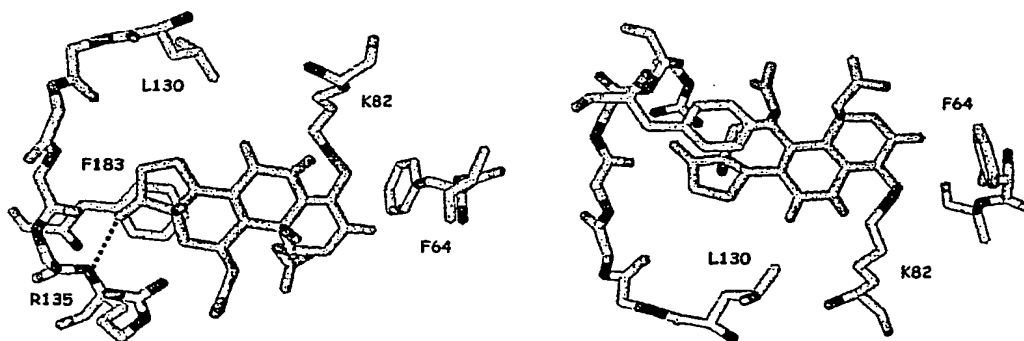


FIGURE 12

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- Control
- ▲ 0.2μM Inhibitor A
- ▼ 0.4μM Inhibitor A
- ◆ 0.8μM Inhibitor A
- 1.6μM Inhibitor A

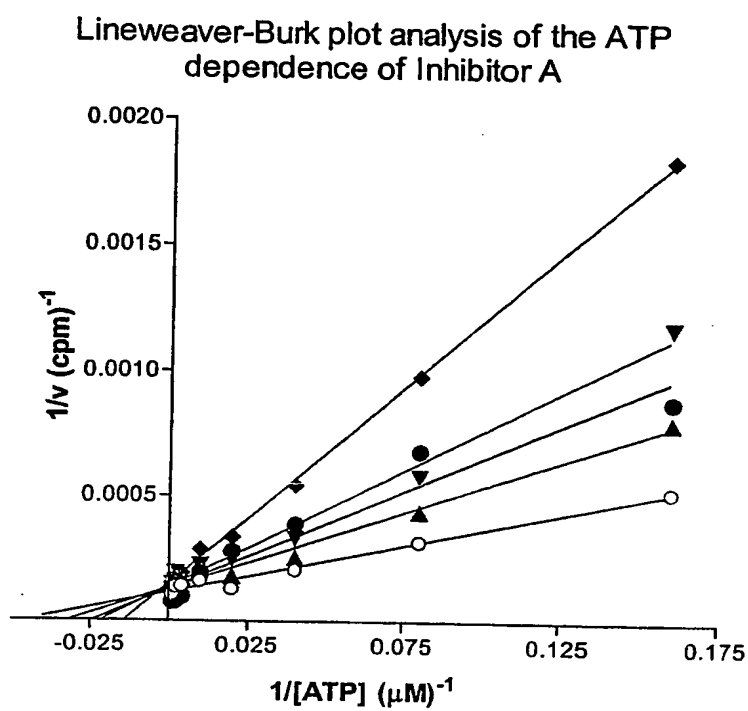


FIGURE 13

(12/13)

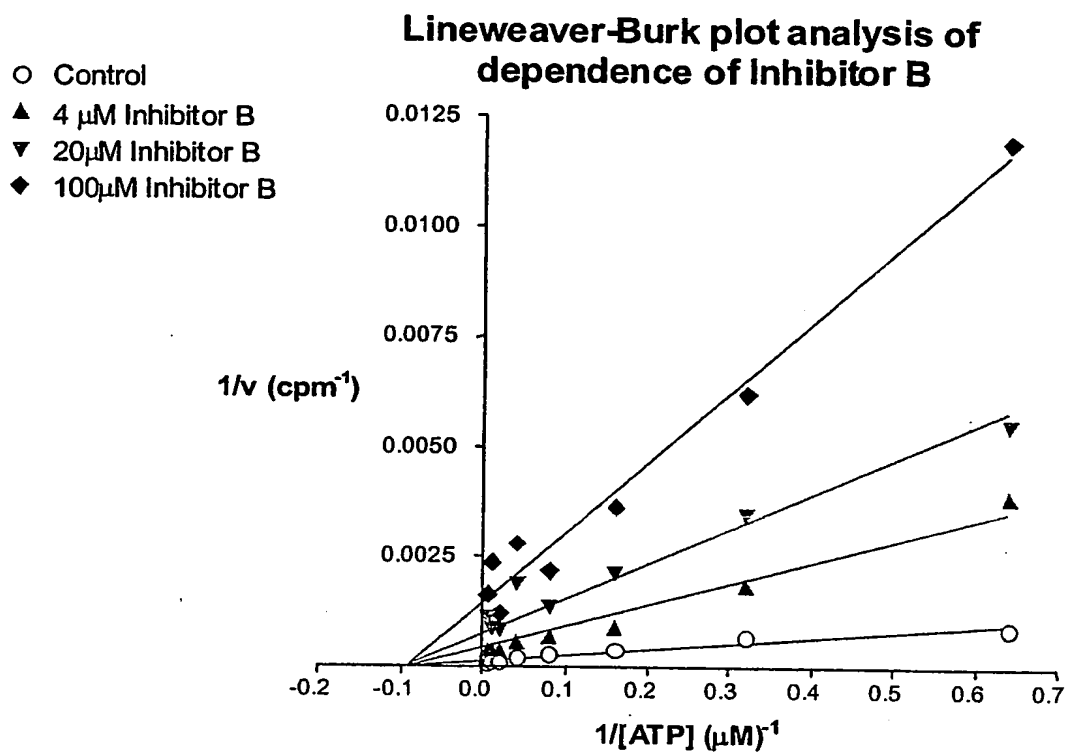


FIGURE 14

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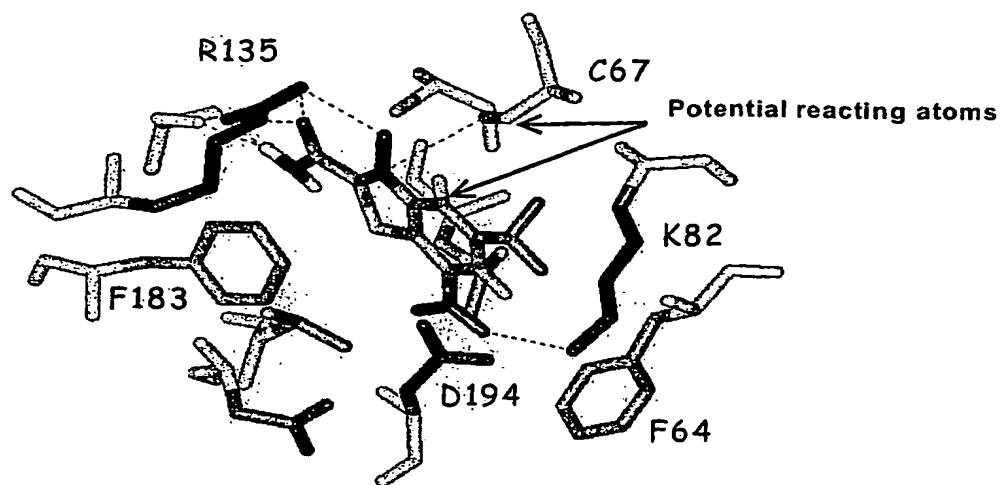


FIGURE 15

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